

WE CLAIM:

1. A cloned bacterial organophosphorus acid anhydrase gene fragment comprising the DNA coding sequence:

5'

ATG CAA ACG AGA AGG GTT GTG CTC TAG TCT GCG GCC GCA GGA ACT CTC CTC GGC  
met gln thr arg arg val val leu lys ser ala ala ala gln thr leu leu gly

GGC CTC GGT GGG TGC GCG ACG TGG CTG GAT CGA TCG GCA CAG GCG ATC GGA TCA  
gly leu ala gly cys ala thr thr leu asp arg ser ala gln ala ile gly ser

ATA CGT GCG CGT CCT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTC ACT CAC GAG  
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu

GAC ATC TGC GGC AGC TCG GCA GGA TTC TCG CGT GCT TCG CCA GAG TTC TTC GGT  
asp ile cys gly ser ser ala gly phe leu arg ala thr pro glu phe phe gly

AGC CGC AAA GGT CTA GCG GAA AAG GCT GTG AGA GGA TTC CGC GCC AGA GCG GGT  
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala

GGC GTG CGA ACG ATT GTC GAT GTC TCG ACT TTC GAT ATC GGT CGC GAC GTC AGT  
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser

TTA TCG GCC GAG GTT TCG CGG GCT GCG GAC ATT CAT ATC GTG GCG GCG ACC GGC  
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly

TTC TCG TTC GAC CGC CCA GTT TCG ATG GCA TTC AGG TAT GTA GAG GAA CTC ACA  
leu thr phe asp pro pro leu ser met arg leu arg tyr val glu glu thr

CAG TTC TTC CTC CGT GAG ATT CAA TAT GGC ATC GAA GAC ACC GGA ATT AGG GCG  
gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala

GGC ATT ATC AAG GTC GCG ACC ACA GCG AAG GCG ACC CGC TTT CAG GAG TTA GTG  
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val

TTA AAG GCG GCG GCG CGG GCG AGC TTC GCG ACC GGT GTT CGC GTA ACC ACT CAC  
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his

ACG GCA GCA AGT CAG CGC GAT GGT GAG CGA GCG AGG CGC CCA TTT TTC AGT CGC  
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro

AAG CTT GAG CGC TCA CGG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTC  
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu

AGC TAT CTC ACC GCG CTC CTC CGC GGA TAC CTC ATC GGT CTA GAC CAC ATC CGC  
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro

CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CGC CTC CTC GCG ATC  
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile

CGT TCG TCG CAA ACA CGG GGT CTC TTC ATC AAG GCG CTC ATC GAC CAA GCG TAC  
arg ser thr gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr

ATG AAA GAA ATC CTC GTT TCG AAT GAC TGG CTC TTC GGG TTT TCG AGC TAT GTC  
met lys gln ile leu val ser asn asp thr leu phe gly phe ser ser tyr val

ACC AAC ATC ATG GAC GTG ATG GAT CGC GTG AAC CGC GAC GGG ATG GCG TTC ATT  
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile

CCA CTC AGA GTG ATC CCA TTC TAC GAG AGA AGG GCG TCG CAC AGG AAA CGC TCG  
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys

CAG GCA TCA CTC TGA  
gln ala ser leu

CTAACCCGCGCGCGTCTCTGTGTCACCGACTTGGCGTGCATGACGCCCATCTGGATCCTTCCACCGCAGCGCGCC  
ACTATTCCCGCTCAAGATACCGAAGCATGAAGTCGCGCATCGATCGATAGGCATCTTCAATGTGATCAGGG  
CTGCGACGCTCAAAAGCCGGTGGCCACCCCTGTTCGATAGTCTTGAGGGACGGTAGCGACGCGGTGCTTTTC  
GTGAACTGCAG

3'

2. The gene fragment of claim 1 wherein said fragment is substantially free of extraneous DNA.

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3. The gene fragment of claim 1 where the DNA is plasmid DNA.

10 4. The gene fragment of claim 1 where the source of the DNA is bacteria of the genus Flavobacterium.

15 5. The gene fragment of claim 1 where the source of the DNA is bacteria of the genus Pseudomonas.

6. An expression vector for producing bacterial organophosphorous acid anhydrase, said vector comprising a cloned bacterial organophosphorus acid anhydrase gene fragment having the DNA coding sequence:

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5'  
CTGCAGCCTGACTCGGACCACTCGGTCGCAAGCAGAGTCCTAAGCAATCCGAGGGGGCAGC  
ATG CAA ACG AGA AGG GTT GTG CTC AAG TCT GCG GCC GCA GGA ACT CTC CTC GGC  
met gln thr arg arg val val leu lys ser ala ala ala gly thr leu leu gly  
GCG CTC GCT GCG TCG GCG ACG TCG CTC GAT CGA TCG GCA CAG GCG ATC GGA TCA  
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser  
ATA GGT GCG GGT GGT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTC ACT CAC GAG  
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu  
GAC ATC TCG GCG AGC TCG GCA GGA TTC TCG GGT GGT TCG CCA GAG TTC TTC GGT  
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly  
AGC GCG AAA GCT CTA GCG GAA AAG GCT GTG AGA GGA TCG GCG GCC AGA GCG GCT  
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala  
GCG CTC CGA ACG ATT GTC GAT GTG TCG ACT TTC GAT ATC GGT GCG GAC GTC AGT  
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser  
TTA TCG GCG GAG GTT TCG GCG GCT GCG GAC GTT CAT ATC GTG GCG GCG ACC GCG  
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly  
TTC TCG TTC GAC GCG CCA CTT TCG ATG CGA TCG AGG TAT GTA GAG GAA CTC ACA  
leu trp phe asp pro pro leu ser met arg leu arg tyr val glu glu leu thr  
CAG TTC TTC CTC GGT GAG ATT CAA GAT GCG ATC GAA GAC ACC GGA ATT AGG GCG  
gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala  
GCG ATT ATC AAG GTC GCG ACC AGA GCG AAG GCG ACC GCG TTC CAG GAG TTA GTC  
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val  
TTA AAG GCG GCG GCG GCG GCG AGC TTC GCG ACC GGT GTT CCG GTA ACC ACT CAC  
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his  
ACG GCA GCA AGT CAG GCG GAT GGT GAG CGA GCG AGG GCG CCA TTT TTC AGT CCG  
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro  
AAG CTT GAG CCG TCA GCG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTC  
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu  
AGC TAT CTC ACC GCG CTC CTC GCG GCA TAC CTC ATC GGT CTA GAC CAC ATC CCG  
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro  
CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CCG CTC CTC GCG ATC  
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile  
CGT TCG TCG CAA ACA CCG GCT CTC TTC ATC AAG GCG CTC ATC GAC CAA GCG TAC  
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr  
ATG AAA CAA ATC CTC GTT TCG AAT GAC TCG CTC TTC GCG TTT TCG AGC TAT GTC  
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val  
ACC AAC ATC ATG GAC GTG ATG GAT CCG GTC AAC CCG GAC GCG ATG GCG TTC ATT  
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile  
CGA CTC AGA GTG ATC CCA TTC TAC GAG AGA AGG GCG TCG CAC AGG AAA CCG TCG  
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys  
CAG GCA TCA CTC TGA  
gln ala ser leu  
CTAACCCTGGCGCGGTCTGTGTCACCGACTTGGCGTGCATGACGCCCATCTGGATCCTTCCACGCGCGCC  
ACTATTCTCCCTCAAGATACCGAACGATGAAGTCGCGCATCGATCGATAGGCATCTTCAATGTGATCAGGG  
CTCCCACTCCAAAGCCGCTGGCCACCCCTGTCTCGATAGTCTTGGGGACCGGTAGCGACCGACCTGCTTTTC  
GTGAAGTCGAG  
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7. The expression vector of claim 6 further comprising a promoter, a start codon, and a recombinant DNA sequence coding for bacterial organophosphorus acid anhydase in accurate reading frame sequence with said start codon for translation.

8. The expression vector of claim 7 wherein said vector is derived from a baculovirus.

9. The expression vector of claim 7 wherein said vector is a bacteriophage.

10. The expression vector of claim 7 wherein said vector is a plasmid.

11. The expression vector of claim 10 wherein said plasmid comprises a transposon capable of transposing the Drosophila genome.

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12. A transformed microorganism comprising an expression vector for producing bacterial organophosphorus acid anhydrase wherein said vector has a cloned bacterial organophosphorus acid anhydrase gene fragment with the DNA coding sequence:

5'  
CTGCAGCCTGACTCGGCGACCCAGTCGCTGCAAGCAGAGTCCTAAGCAATGCGAAGGGGGCAGC  
ATG CAA ACG AGA AGG GTT GTG CTC AAG TCT GCG GCC GCA GGA ACT CTG CTC GGC  
met gln thr arg arg val val leu lys ser ala ala ala gly thr leu leu gly  
GGC CTG GGT GGG TGC GCG ACG TGG CTG GAT CSA TCG GCA CAG GCC ATC GGA TCA  
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser  
ATA CGT GCG CGT CCT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTG ACT CAC GAG  
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu  
GAC ATC TGC GGC AGC TCG GCA GGA TTC TTG CGT GCT TGG CCA GAG TTC TTC GGT  
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly  
AGC CGC AAA GCT CTA GCG GAA AAG GCT GTG AGA GGA TTG CGC GCC AGA GCG GCT  
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala  
GGC GTG CGA ACG ATT GTC GAT GTG TCG ACT TTC GAT ATC GGT CGC GAC CTC AGT  
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser  
TTA TTG GCC GAG GTT TCG CGG GCT GCC GAC GTT CAT ATC GTG GCG GCG ACC GGC  
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly  
TTG TGG TTC GAC CGC CCA CTT TCG ATG CGA TTG AGG TAT GTA GAG GAA CTC ACA  
leu trp phe asp pro pro leu ser met arg leu arg tyr val glu leu thr  
CAG TTC TTC CTG CGT GAG ATT CAA TAT GGC ATC GAA GAC ACC GGA ATT AGG GCG  
gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala  
GGC ATT ATC AAG CTC GCG ACC ACA GCG AAG GCG ACC CGC TTT CAG GAG TTA GTG  
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val  
TTA AAG GCG GCC GCG CGC GCG GCC AGC TTG GCC ACC GGT GTT CGC GTA ACC ACT CAC  
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his  
ACG GCA GCA AGT CAG CGC GAT GGT GAG CGA GCG AGG CGC CCA TTT TTG AGT CGG  
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro  
AAG CTT GAG CCC TCA CGG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTG  
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu  
AGC TAT CTC ACC GCC CTG CTG CGC GGA TAC CTC ATC GGT CTA GAC CAC ATC CGC  
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro  
CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CGC CTC CTG GCG ATC  
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile  
CGT TCG TGG CAA ACA CGG GCT CTC TTG ATC AAG GCG CTC ATC GAC CAA GGC TAC  
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr  
ATG AAA CAA ATC CTC GTT TCG AAT GAC TGG CTG TTC GGG TTT TCG AGC TAT GTC  
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val  
ACC AAC ATC ATG GAC GTG ATG GAT CGC GTG AAC CCC GAC GGG ATG GCC TTC ATT  
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile  
CCA CTG AGA GTG ATC CCA TTC TAC GAG AGA AGG GCG TCC CAC AGG AAA CGC TGC  
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys  
CAG GCA TCA CTG TGA  
gln ala ser leu  
CTAACCCTGGCGCGGTCTGTGTGTCACCGACTTGCCTGCGATGACGCCATCTGGATCCTTCCACGCGAGCGGCC  
ACTATTCTCCCGTCAAGATACCGAAGCATGAAGTCCGCGCATCGATCGATAGGCATCTTCAATGTGATCAGGG  
CTGCCACCTCCAAAGCCGGTGGGCCACCCCTGTGCGATAGTCTTGGAGGACCGGTAGCGACGACCGCTGCTTTTC  
GTGAACGCGAG  
3'

13. The transformed microorganism of claim 12 wherein said microorganism is a bacteria.

14. A transformed eukaryotic cell line comprising an expression vector for producing bacterial organophosphorus acid anhydrase wherein said vector has a cloned bacterial organophosphorus acid anhydrase gene fragment with the DNA coding sequence:

5'  
CTGCAGCCTGACTCGGACCCAGTCGCTGCAAGCAGAGTCGTAAGCAATCCCAAGGGGGCAGC  
ATG CAA ACG AGA AGG GTT GTG CTC AAG TCT GCG GCC GCA GGA ACT CTC CTC GGC  
met gln thr arg val val val leu lys ser ala ala ala gly thr leu leu gly  
GGC CTC GGT GCG TGC GCG ACG TGG CTC GAT CCA TCG GCA CAG GCG ATC GGA TCA  
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser  
ATA CGT GCG CGT CCT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTC ACT CAC GAG  
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu  
GAC ATC TCG GCG AGC TCG GCA GGA TTC TCG CGT GGT TGG CCA GAG TTC TTC GGT  
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly  
AGC GCG AAA GCT CTA GCG GAA AAG GCT GTC AGA GGA TTC GCG GCC AGA GCG GCT  
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala  
GGC GTC CCA ACG ATT GTC GAT GTG TCG ACT TTC GAT ATC GGT GCG GAC GTC AGT  
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser  
TTA TTC GCG GAG GTT TCG GCG GGT GCG GAC GTT CAT ATC CTC GCG GCG ACC GCG  
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly  
TTC TGG TTC GAC GCG CCA CTT TCG ATG CCA TTC AGG TAT GTA GAG GAA CTC ACA  
leu trp phe asp pro pro leu ser met arg leu arg tyr val glu glu leu thr  
CAG TTC TTC CTC GGT GAG ATT CAA TAT GGC ATC GAA GAC ACC GGA ATT AGG GCG  
gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala  
GGC ATT ATC AAG GTC GCG ACC ACA GCG AAG GCG ACC GCG TTC CAG GAG TTA CTC  
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val  
TTA AAG GCG GCG GCG GCG GCG ACC TTC GCG ACC GGT GTT GCG GTA ACC ACT CAC  
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his  
ACG GCA GCA AGT CAG CCG GAT GGT GAG CCA GCG AGG GCG CCA TTC TTC AGT GCG  
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro  
AAG CTT GAG CTT TCA GCG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTC  
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu  
AGC TAT CTC ACC GCG CTC CTC GCG GGA TAC CTC ATC GGT CTA GAC CAC ATC GCG  
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro  
CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CCG CTC CTC GCG ATC  
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile  
CGT TCG TCG CAA ACA CCG GGT CTC TTC ATC AAG GCG CTC ATC GAC CAA GCG TAC  
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr  
ATG AAA CAA ATC CTC GTT TCG AAT GAC TCG CTC TTC GCG TTC TCG AGC TAT GTC  
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val  
ACC AAC ATC ATG GAC GTG ATG GAT CCG GTG AAC CCG GAC GCG ATG GCG TTC ATT  
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile  
CCA CTC AGA GTG ATC CCA TTC TAC GAG AGA AGG GCG TCG CAC AGG AAA CCG TCG  
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys  
CAG GCA TCA CTC TGA  
gln ala ser leu  
CTAACCGCGCGCGGTCTGTGTGTCACCGAAGTTCGCGTGCATGACGCCATCTGGATCCTTCCACCGCAGCGCGC  
ACTATTCGCGCGTCAAGATACCGAAGCATGAAGTCGCGCATCGATCGATAGGCATCTTCAATGTGATCAGGG  
CTGCGACCTTCAAAAGCGCGGTGCGCCACCGCTGTGATAGTCTTGAGGACCGGTAGCGACCGGTGCTTTTC  
GTGAAGTGCAG  
3'

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15. The transformed cell line of claim 14 wherein said cell line is derived from an insect.

5 16. The transformed cell line of claim 15 wherein said insect is a Fall army worm caterpillar.

5'  
CTGCAGCCTGACTGGGACCACTGCTGCTCAAGCAGAGTCTGAAGCAATGCAAGGGGGGAGG  
ATG CAA ACG AGA AGG GTT GTG CTC AAG TCT GCG GCC GCA GGA ACT CTC CTC GGC  
met gln thr arg arg val val leu lys ser ala ala ala gly thr leu leu gly  
GGC CTC GGT GGG TGC GCG ACG TGG CTC GAT CGA TCG GCA CAG GCG ATC GGA TCA  
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser  
ATA CGT GCG CGT COT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTC ACT CAC GAG  
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu  
GAC ATC TCG GGC AGC TCG GCA GGA TTC TTS CGT GGT TGG CGA GAG TTC TTC GGT  
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly  
AGC CGC AAA GGT CTA GCG GAA AAG GGT GTG AGA GGA TTS CGC GCC AGA GCG GGT  
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala  
GGC GTG CGA ACG ATT GTC GAT GTG TCG ACT TTC GAT ATC GGT CGC GAC CTC AGT  
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser  
TTA TCG GCG GAG GTT TCG CCG GGT GCG GAC GTT CAT ATC GTG GCG GCG ACC GCG  
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly  
TTS TCG TTC GAC CGC CGA CTT TCG ATG CGA TTS AGG TAT GTA GAG GAA CTC ACA  
leu trp phe asp pro pro leu ser met arg leu arg tyr val glu glu leu thr  
CAG TTC TTC CTC GGT GAG ATT GAA TAT GGC ATC GAA GAC ACC GGA ATT AGG GCG  
gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala  
GGC ATT ATC AAG GTC GCG ACC ACA GCG AAG GCG ACC CGC TTT CAG GAG TTA GTG  
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu val  
TTA AAG GCG GCG GCG GCG GCG AGC TTS GCG ACC GGT GTT CGC GTA ACC ACT CAC  
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his  
ACG GCA GCA AGT CAG CGC GAT GGT GAG CGA GCG AGG CGC CGA TTT TTS AGT CGC  
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro  
AAG CTT GAG CGC TTA CCG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTS  
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu  
AGC TAT CTC ACT GCG CTC CTC CCG GGA TAC TTC ATC GGT CTA GAC CAC ATC CGC  
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro  
CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CGC CTC CTC GCG ATC  
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile  
CGT TCG TGG CAA ACA CCG GGT CTC TTS ATC AAG GCG CTC ATC GAC CAA GCG TAC  
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr  
ATG AAA CAA ATC CTC GTT TCG AAT GAC TGG CTC TTC GCG TTT TCG AGC TAT GTC  
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val  
ACC AAC ATC ATG GAC GTG ATG GAT CGC GTG AAC CGC GAC GCG ATG GCG TTC ATT  
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile  
GCA CTC AGA GTG ATC CGA TTC TAC GAG AGA AGG GCG TCG CAC AGG AAA CCG TCG  
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys  
CAG GCA TCA CTC TGA  
gln ala ser leu  
CTAAGCCCGGCGGGTCTGTGTGTCACCGACTTGGCGGTGCGATGACCGCATCTGGATCTTCCACCGAGCGGGC  
ACTATTCCCGCTCAAGATACCGAACGATGAAGTCCCGCATGATCGATAGGCATCTTCAATGTGATCAGGG  
CTGCGACCTCCAAAGCCGGTGGCCACCGCTGTGATAGTCTTTGAGGGACCGGTAGCCACGACCGTCTGCTTTTC  
GTGAAGCTGCAG  
3'

17. A transgenic eukaryotic organism comprising an expression vector for producing bacterial organophosphorus acid anhydrase wherein said vector has a cloned bacterial organophosphorus acid anhydrase gene fragment having the
- 5 DNA coding sequence:

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5'
CTSCAGCGCTGACTCGGACCCAGTCCGCTCCAAAGCAGAGTCTTAAGCAATCCCAAGGGGGCAGC
ATG CAA ACG AGA AGG GTT GTG CTC AAG TCT GCG GCC GCA GGA ACT CTG CTC GCG
met gln thr arg arg val leu lys ser ala ala ala gly thr leu leu gly
GGC CTG GGT GGG TGC GCG ACG TGG CTG GAT CGA TCG GCA CAG GCG ATC GGA TCA
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser
ATA CGT GCG CGT CCT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTG ACT CAC GAG
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu
GAC ATC TGC GGC AGC TCG GCA GGA TTC TCG CGT GGT TGG CCA GAG TTC TTC GGT
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly
AGC CGC AAA GCT CTA GCG GAA AAG GCT GTG AGA GGA TTC CGC GCC AGA GCG GCT
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala
GGC GTG CGA ACG ATT GTC GAT GTG TCG ACT TTC GAT ATC GGT CGC GAC GTC AGT
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser
TTA TTC GCC GAG GTT TCG CGC GCT GCC GAC GTT CAT ATC CTG GCG GCC ACC GCG
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly
TTC TGG TTC GAC CGC CCA CTT TCG ATG CGA TTC AGG TAT ATA GAG GAA CTC ACA
leu trp phe asp pro pro leu ser met arg leu arg tyr val glu glu leu thr
CAG TTC TTC CTG CGT GAG ATT CAA TAT GGC ATC GAA GAC ACC GGA ATT AGG GCG
gln phe phe leu arg glu ile gln tyr gly ala glu asp thr gly ile arg ala
GGC ATT ATC AAG GTC GCG ACC ACA GCG AAG GCA ACC CGC ATT CAG GAG TTA GTG
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val
TTA AAG GCG GCC CGC CGC GCG ACC TTC GCG ACC GGT GGT CGC GTA ACC ACT CAC
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his
ACC GCA GCA AGT CAG CGC GAT GGT GAG CGA GCG AGG CGC CCA TTT TTC AGT CGC
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro
AAG CTT GAG CGC TCA CGC GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTC
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu
AGC TAC CTC ACC GCG CTG CTG CGC GGA TAC CTC ATC GGT CTA GAC CAC ATC CGC
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro
CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CGC CTC CTG GCG ATC
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile
CGT TCG TGG CAA ACA CGC GGT CTC TTC ATC AAG GCG CTC ATC CAC CAA GCG TAC
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr
ATG AAA CAA ATC CTC GTT TCG AAT GAC TGG CTG TTC GGG TTT TCG AGC TAT GTC
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val
ACC AAC ATC ATG GAC GTG ATG GAT CGC GTG AAC CGC GAC GGG ATG GCG TTC ATT
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile
CCA CTG AGA GTG ATC CCA TTC TAC GAG AGA AGG GCG TCG CAC AGG AAA CGC TCG
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys
CAG GCA TCA CTC TGA
gln ala ser leu
CTAACCGCGCGCGGTCTGTGTCACCGAAGTTCGCGTGCATGACCGCCATCTGGATCCTTCCACGCGAGCGGCC
ACTATTCGCGCGTCAAGATACCGAAGCATGAAGTCGCGCATCGATAGGCATCTTCAATGTGATCAGGG
CTGCGACCTCCAAAGCGCGGTGGCGCACCGCTGTGTCATAGTCTTGGAGGACCGGTAGCGACCGACCGTGTCTTC
GTGAAGTGCAG
3'
```



18. A transgenic organism as claimed in claim 17 wherein  
said organism is derived from microinjection of said  
expression vector into Drosophila melanogaster embryo  
5 cells.

Csm

19. A transgenic organism as claimed in claim 17 wherein  
said organism is derived from injection of said expression  
10 vector into a Fall army worm caterpillar.

20. A method for making bacterial organophosphorus acid  
anhydrase, said method comprising:

15

growing in a nutrient medium a transformed  
microorganism having an expression vector with a  
cloned bacterial organophosphorus acid anhydrase  
gene fragment having the DNA coding sequence:

20

5' CTGCAGCCTGACTCGGCACCACTGCTGCTGCAAGCAGAGTCTGTAAGCAATCGCAAGGGGGCAGC  
 ATG CAA ACC AGA AGG GTT GTG CTC AAG TCT GCG GCC GCA GGA ACT CTG CTC GGC  
 met gln thr arg arg val val leu lys ser ala ala ala gly thr leu leu gly  
 5 GGC CTG GCT GGG TGC GCG ACC TGG CTG GAT GSA TGG GCA CAG GCG ATC GGA TCA  
 gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser  
 ATA CGT GCG CGT CCT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTG ACT CAC GAG  
 ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu  
 GAC ATC TGC GGC AGC TCG GCA GGA TTC TGG CGT GGT TGG CCA GAG TTC TTC GGT  
 asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly  
 AGC CGC AAA GCT CTA GCG GAA AAG GCT GTG AGA GGA TTC CGC GCC AGA GCG GCT  
 ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala  
 10 GGC GTG CGA ACC ATT GTC GAT GTG TCG ACT TTC GAT ATC GGT CGC GAC GTC AGT  
 gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser  
 TTA TTG GCG GAG GTT TCG CGG GCT GCG GAT CAT ATC GTG GCG ACC GCG  
 leu leu ala glu val ser arg ala ala asp val his ile val ala thr gly  
 TTG TGG TTC GAC CGC CCA CTT TGG ATG GGA TTG AGG TAT GTA GAG GAA CTC ACA  
 leu trp phe asp pro pro leu ser met arg leu arg tyr val glu glu leu thr  
 CAG TTC TTC CTG CGT GAG ATT CAA TAT GGC ATC GAA GAC ACC GGA ATT AGG GCG  
 gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala  
 15 GGC ATT ATC AAG GTC GCG ACC ACA GCG AAG GCG ACC CGC TTC CAG GAG TTA GTG  
 gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val  
 TTA AAG GCG GCG GCG GCG GCG AGG TTG GCG ACC GGT GTT CCG GTA ACC ACT CAC  
 leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his  
 ACC GCA GCA AGT CAG CGC GAT GGT GAG CGA GCG AGG CGC CCA TTC TTG AGT CGC  
 thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro  
 AAG CTT GAG CGC TCA CGG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTG  
 lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu  
 AGC TAT CTC ACC GCG CTG CTG CGC GGA TAC CTC ATC GGT CTA GAC CAC ATC CGC  
 ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro  
 20 CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CGC CTC CTG GCG ATC  
 his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile  
 CGT TCG TGG CAA ACA CGG GCT CTC TTG ATC AAG GCG CTC ATC GAC CAA GCG TAC  
 arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr  
 ATG AAA CAA ATC CTC GTT TCG AAT GAC TGG CTG TTC GCG TTC TCG AGC TAT GTC  
 met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val  
 ACC AAC ATC ATG GAC GTG ATG GAT CGC GTG AAC CGC GAC GCG ATG GCG TTC ATT  
 thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile  
 25 CCA CTG AGA GTG ATC CCA TTC TAC CAG AGA AGG GCG TCC CAC AGG AAA GCG TGC  
 pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys  
 CAG GCA TCA CTG TGA  
 gln ala ser leu  
 CTAACCGGGCGCGGCTTCTGTGTCACCGAATTGCGCTGCGATGACCGCATCTGGATCCTTCCAGCGAGCGGGC  
 ACTATTCCCGCTCAAGATACCGAAGCATGAAGTCGCGCATCGATCGATAGGCATCTTCAATGTGATCAGGG  
 CTCCACCTCCAAAGCCGGTGGCCACCCCTGTGCGATAGTCTTGAGGGACCGGTAGCGACGACCGCTGCTTTC  
 GTGAAGTGCAG  
 3'

allowing said microorganism to produce bacterial  
 organophosphorus acid anhydrase; and

recovering the bacterial organophosphorus acid  
 anhydrase.

21. A method for making bacterial organophosphorus acid anhydrase, said method comprising:

growing in a nutrient medium a transformed eukaryotic cell line comprising an expression vector with a cloned bacterial organophosphorus acid anhydrase gene fragment having the DNA coding sequence:

5' CTGCAGCCTGACTCGGCGCCAGTCCGCTGCAAGCAGAGTCGTAAGCAATCCCAAGGGGGCAGC  
ATG CAA ACG AGA AGG GTT GTG ATC AAG TCT GCG GCC GCA GGA ACT CTG CTC GGC  
10 met gln thr arg arg val val leu lys ser ala ala ala gly thr leu leu gly  
GGC CTG GCT GGG TGC GCG ACC TGG CTG GAT CGA TCG GCA CAG GCG ATC GGA TCA  
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser  
ATA CGT GCG CGT CCT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTG ACT CAC GAG  
15 ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu  
GAC ATC TGC GGC AGC TCG GCA GGA TTC TTA CGT GCT TGG CCA GAG TTC TTC GGT  
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly  
AGC GCG AAA GCT CTA GCG GAA AAG GCT GTG AGA GGA TTG CCG GCC AGA GCG GCT  
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala  
20 GGC CTG CGA ACG ATT GTC GAT GTG TCG ACT TTC GAT ATC GGT GCG GAC GTC AGT  
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser  
TTA TTG GCG GAG GTT TCG CGG GCT GCG GAC GTT CAT ATC GTG GCG GCG ACC GCG  
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly  
TTG TGG TTC GAC CGC CCA GTT TCG ATG CGA TTG AGG TAT GTA GAG GAA CTC ACA  
leu trp phe asp pro pro leu ser met arg leu arg tyr val glu glu leu thr  
CAG TTC TTC CTG CGT GAG ATT CAA TAT GCG ATC GAA GAC ACC GGA ATT AGG GCG  
25 gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala  
GGC ATT ATC AAG GTC GCG ACC ACA GCG AAG GCG ACC GCG TTT CAG GAG TTA GTG  
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val  
TTA AAG GCG GCG GCG GCG GCG ACC TTC GCG ACC GGT GTT CCG GTA ACC ACT CAC  
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his  
ACG GCA GCA AGT CAG CGC GAT GGT GAG CGA GCG AGG GCG CCA TTT TTG AGT CCG  
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro  
AAG CTT GAG CCG TCA CGG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTG  
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu  
30 AGC TAT CTC ACC GCG CTG CTG CCG GGA TAC CTC ATC GGT CTA GAC CAC ATC CCG  
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro  
CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CCG CTC CTG GCG ATC  
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile  
CGT TCG TGG CAA ACA CGG GCT CTC TTG ATC AAG GCG CTC ATC GAC CAA GCG TAC  
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr  
ATG AAA CAA ATC CTC GTT TCG AAT GAC TGG CTG TTC GCG TTT TCG AGC TAT GTC  
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val  
ACC AAC ATC ATG GAC GTG ATG GAT CCG GTG AAC CCG GAC GGG ATG GCG TTC ATT  
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile  
CCA CTG AGA GTG ATC CCA TTC TAC GAG AGA AGG GCG TCC CAC AGG AAA CCG TCG  
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys  
CAG GCA TCA CTG TGA  
gln ala ser leu  
CTAACCCCGCGCGGTTCTGTGTGTCACCGACTTGGCGGTGCATGACGCCATCTGGATCCTTCCACCGAGCGGCG  
ACTATTCGCGCGCTCAAGATACCGAAGCATGAAAGTCGCGCATCGATCGATAGGCGATCTTCAATGTGATCAGGG  
CTGCGACCTCCAAAGCGCGTGGCCACCGCTGTGATAGTCTTGGAGGCGCGTAGCGACGACCGCTGCTTTC  
GTGAAGTGCAG  
3'

allowing said microorganism to produce bacterial  
organophosphorus acid anhydrase; and

recovering the bacterial organophosphorus acid  
anhydrase.

5

22. A method for making bacterial organophosphorus acid anhydrase, said method comprising:

5       nourishing a transformed host in a nutrient medium  
          allowing said host to produce bacterial  
          organophosphorus acid anhydrase;

10       transforming host an expression vector comprising a  
          DNA sequence coding for said bacterial  
          organophosphorus acid anhydrase; and

15       separating the bacterial organophosphorus acid  
          anhydrase from said host and said nutrient  
          medium.

20       23. The method for making bacterial organophosphorus acid  
          anhydrase of claim 22 further comprising purifying said  
          bacterial organophosphorus acid anhydrase.

25       24. The method for making bacterial organophosphorus acid  
          anhydrase of claim 22 wherein said host is a  
          microorganism.

30       25. The method for making bacterial organophosphorus acid  
          anhydrase of claim 24 wherein said microorganism is a  
          bacteria.

35       26. The method for making bacterial organophosphorus acid  
          anhydrase of claim 22 wherein said host is a eukaryotic  
          cell line.

27. The method for making bacterial organophosphorus acid anhydrase of claim 26 wherein said eukaryotic cell line is derived from an insect.

5

28. The method for making bacterial organophosphorus acid anhydrase of claim 27 wherein said insect is a Fall army worm caterpillar.

10

29. The method of claim 22 wherein said anhydrase is purified to a level of approximately 3200 units/mg of anhydrase.

15

30. The cloned bacterial organophosphorus acid anhydrase gene fragment of claim 1 where in the N-terminal sequence up to the start codon has been deleted from said DNA coding sequence.

20

31. The expression vector of claim 6 wherein the N-terminal sequence up to the start codon has been deleted from said DNA coding sequence.

25

32. The transformed microorganism of claim 12 wherein the N-terminal sequence up to the start codon has been deleted from said DNA coding sequence.

30

33. The transformed eukaryotic cell line of claim 14 wherein the N-terminal sequence up to the start codon has been deleted from said DNA coding sequence.

35

34. The transgenic eukaryotic organism of claim 17 wherein the N-terminal sequence up to the start codon has been deleted from said DNA coding sequence.

5

35. The method for making bacterial organophosphorus acid anhydrase of claim 20 wherein the N-terminal sequence up to the start codon has been deleted from said DNA coding sequence.

10

36. The method for making bacterial organophosphorus acid anhydrase of claim 21 wherein the N-terminal sequence up to the start codon has been deleted from said DNA coding sequence.

15

37. The cloned bacterial organophosphorus acid anhydrase gene fragment of claim 1 wherein the C-terminal sequence has been deleted from Bam HI to PstI of said DNA coding sequence.

20

38. The expression vector of claim 6 wherein the C-terminal sequence has been deleted from Bam HI to PstI of said DNA coding sequence.

25

39. The transformed microorganism of claim 12 wherein the C-terminal sequence has been deleted from Bam HI to PstI of said DNA coding sequence.

30

*Sub 13*  
40. The transformed eukaryotic cell line of claim 14 wherein the C-terminal sequence has been deleted from Bam HI to PstI of said DNA coding sequence.

5  
41. The transgenic eukaryotic organism of claim 17 wherein the C-terminal sequence has been deleted from Bam HI to PstI of said DNA coding sequence.

10  
42. The method for making bacterial organophosphorus acid anhydase of claim 20 wherein the C-terminal sequence has been deleted from Bam HI to PstI of said DNA coding sequence.

15  
43. The method for making bacterial organophosphorus acid anhydase of claim 21 wherein the C-terminal sequence has been deleted from Bam HI to PstI of said DNA coding  
20 sequence.

44. Organophosphorus acid anhydase produced by a genetically transformed host having an expression vector  
25 comprising a DNA sequence coding for said anhydase.

*improp. dependent claim. no ante content basis for the method*  
45. The method of claim 44 wherein said anhydase is characterized by  $K_{cat} = 2100 \text{ sec}^{-1}$  for paraoxon.  
30



46. Bacterial organophosphorus acid anhydrase produced by a genetically transformed host having an expression vector comprising a cloned gene fragment with the DNA coding sequence:

5

```

5'
CTGCAGCCCTGACTCGGCACCAGTCCGCTCCAGCAGAGTCTTAAGCAATCCCAAGGGGGCAGC
ATG CAA ACG AGA AGG GTT GTG CTC AAG TCT GCG GCC GCA GGA ACT CTC CTC GGC
met gln thr arg arg val val leu lys ser ala ala ala gly thr leu leu gly

GGC CTC GGT GGG TGC GCG ACG TGG CTG GAT CGA TCG GCA CAG GCG ATC GGA TCA
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser

ATA CGT GCG CGT CCT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTC ACT CAC GAG
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu

GAC ATC TGC GGC AGC TCG GCA GGA TTC TCG GGT GGT TCG CCA GAG TTC TTC GGT
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly

AGC CGC AAA GCT CTA GCG GAA AAG GGT GTG AGA GGA TTC CGC GCC AGA GCG GCT
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala

GGC GTG CGA ACG ATT GTC GAT GTG TCG ACT TTC GAT ATC GGT CGC GAC GTC AGT
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser

TTA TTC GCG GAG GTT TCG CGG GCT GCC GAC GTT CAT ATC GTG GCG GCG ACC GGC
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly

TTG TGG TTC GAC CCG CCA CTT TCG ATG CGA TTC AGG TAT GTA GAG GAA CTC ACA
leu trp phe asp pro pro leu ser met arg leu arg tyr val glu glu leu thr

CAG TTC TTC CTC COT GAG ATT CAA TAT GGC ATC GAA GAC ACC GCA ATT AGG GCG
gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala

GGC ATT ATC AAG GTC GCG ACC ACA GCG AAG GCG ACC CGC TTT CAG GAG TTA GTG
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val

TTA AAG GCG GCC GCG CGG GCC AGC TTC GCG ACC GGT GTT CCG GTA ACC ACT CAC
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his

ACG GCA GCA AGT CAG CGC GAT GGT GAG CGA GGC AGG CCG CCA TTT TTG AGT CCG
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro

AAG CTT GAG CCC TCA CGG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTC
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu

AGC TAT CTC ACC GCC CTC CTC CGC GGA TAC CTC ATC GGT CTA GAC CAC ATC CCG
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro

CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CCG CTC CTC GGC ATC
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile

CGT TCG TGG CAA ACA CGG GGT CTC TTG ATC AAG GCG CTC ATC GAC CAA GCG TAC
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr

ATG AAA CAA ATC CTC GTT TCG AAT GAC TCG CTC TTC GCG TTT TCG AGC TAT GTC
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val

ACC AAC ATC ATG GAC GTG ATG GAT CGC GTG AAC CCC GAC GGG ATG GCG TTC ATT
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile

CCA CTC AGA GTG ATC CCA TTC TAC GAG AGA AGG GCG TCC CAC AGG AAA CCG TCG
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys

CAG GCA TCA CTC TGA
gln ala ser leu
CTAACCCGGCGCGGTCTGTGTCACCGACTTGCCTGTCATGACGCCATCTGGATCCTTCCACGAGCGGCC
ACTATTCCTCCGTCAAGATACCGAACGATGAAGTCGCGCATCGATCGATAGGCATCTTCAATGTGATCAGGG
CTGCCACCTCCAAAGCCCGTGGCCACCCCTGTCTGATAGTCTTGGAGGACCGGTAGCGACGACCGTCTTTTC
GTGAACCTGCAG
3'

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47. The bacterial organophosphorus acid anhydrase of claim 46 wherein the N-terminal sequence up to the start codon has been deleted from said DNA coding sequence.

48. The bacterial organophosphorus acid anhydrase of claim 46 wherein the C-terminal sequence up to the start codon; has been deleted from Bam HI to PstI of said DNA coding sequence.

49. The bacterial organophosphorus acid anhydrase of claim 46 wherein said host producing acid anhydrase is a microorganism.

50. The bacterial organophosphorus acid anhydrase of claim 46 wherein said host producing said anhydrase is a bacterial.

51. The bacterial organophosphorus acid anhydrase of claim 46 wherein said host is a eukaryotic cell line.

52. The bacterial organophosphorus acid anhydrase of claim 46 wherein said anhydrase is relatively pure, characterized by  $K_{cat} = 2100 \text{ sec}^{-1}$  for paraoxon.

53. A method for detoxifying an organophosphorus compound comprising exposing said compound to recombinant bacterial organophosphorus acid anhydrase.

54. The method of claim 53 wherein said exposure is accomplished by passing said compound through a matrix comprising said recombinant anhydrase.

5

55. The method of claim 54 wherein said matrix is further comprised of a filtration device.

10 56. The method of claim 55 wherein said device is a gas mask.

15 57. The method of claim 53 wherein said organophosphorus compound is in air.

20 58. The method of claim 53 wherein said organophosphorus compound is in a fluid.

25 59. The method of claim 53 wherein said exposure is accomplished by spraying said recombinant anhydrase on a locus comprising the organophosphorus compound.

30 60. The method of claim 53 wherein said exposure is accomplished by introducing said anhydrase into a container comprising the organophosphorus compound.

61. The method of claim 53 wherein said recombinant bacterial organophosphorus acid anhydrase is produced by a transformed microorganism comprising an expression vector for producing said anhydrase and wherein said vector has a
- 5 cloned bacterial organophosphorus acid anhydrase gene fragment with the DNA coding sequence:

5'  
CTGCAGCCTGACTCGGCACCACTCGCTGCAAGCAGAGTCCTAAGCAATCGCAAGGGGSCAGC  
ATG CAA ACG AGA AGG GTT GTG CTC AAG TCT TCG GCC GCA GGA ACT CTG CTC GGC  
met gln thr arg arg val val leu lys ser ala ala ala gly thr leu leu gly  
GGC CTG GCT GGG TGC GCG ACG TGG CTG GAT CGA TCG GCA CAG GCG ATC GGA TCA  
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser  
ATA CGT GCG CGT CCT ATC AGA ATC TCT GAA GCG GGT TTC ACA CTG ACT CAC GAG  
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu  
GAC ATC TGC GGC AGC TCG GCA GGA TTC TTG GGT GCT TGG CCA GAG TTC TTC GGT  
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly  
AGC CGC AAA GCT GTA GCG GAA AAG GGT GTG AGA GGA TTG CGC GCC AGA GCG GCT  
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala  
GGC GTG CGA ACG ATT GTC GAT GTG TCG ACT TTC GAT ATC GGT CGC GAC CTC AGT  
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser  
TTA TTG GGC GAG GTT TCG CCG GGT GGC GAC GTT CAT ATC GTG GCG GCG ACC GGC  
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly  
TTG TGG TTC GAC CCG CGA CTT TCG ATG CGA TTG AGG TAT GTA GAG GAA CTC ACA  
leu trp phe asp pro pro leu ser met arg leu arg tyr val glu glu leu thr  
CAG TTC TTC CTG GGT GAG ATT CAA TAT GGC ATC GAA GAC ACC GGA ATT AGG GCG  
gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala  
GGC ATT ATC AAG GTC GCG ACC ACA GGC AAG GCG ACC CGC TTT CAG GAG TTA GTG  
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val  
TTA AAG GCG GCC GCG CCG GCT AGC TTG GCG ACC GGT GTT CCG GTA ACC ACT CAC  
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his  
ACG GCA GCA AGT CAG CCG GAT GGT GAG CGA GCG AGG CGC CGA TTT TTG AGT CGC  
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro  
AAG CTT GAG CCG TCA CCG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTG  
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu  
AGC TAT CTC ACC GCC CTG CTG CCG CGA TAC CTC ATC GGT CTA GAC CAC ATC CGC  
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro  
CAC AGT GCG ATT GGT TTA GAA GAT AAT GCG AGT GCA TCA CCG CTC CTG GGC ATC  
his ser ala ile gly leu glu asp asp ala ser ala ser pro leu leu gly ile  
CST TCG TGG CAA ACA CCG GCT CTG TTG ATC AAG GCG CTC ATC GAC CAA GGC TAC  
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr  
ATG AAA CAA ATC CTC GTT TCG AAT GAC TGG CTG TTC GGG TTT TCG AGC TAT GTC  
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val  
ACC AAC ATC ATG GAC GTG ATG GAT CCG GTG AAC CCG GAC GGG ATG GCG TTC ATT  
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile  
CCA CTG AGA GTG ATC CCA TTC TAC GAG AGA AGG GCG TCC CAC AGG AAA CCG TCG  
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys  
CAG GCA TCA CTG TGA  
gln ala ser leu  
CTAACCCGGCGCGGTCTGTGTACCGGACTTGGCGCTGCATGACGCCATCTGGATCCTTCCACCGCAGCGGCC  
ACTATTCCTCCGTCAAGATACCGAACGATGAAGTCGCGCATCGATCGATAGGCATCTTCAATGTGATCAGGG  
CTGCCACCTCCAAAGCCGGTGGCCACCCCTGTGCGATAGTCTTGGAGGACGGTAGCGACCGGTGCTTTTC  
GTGAACCTGAC  
3'

62. The method of claim 53 wherein said recombinant bacterial organophosphorus acid anhydrase is produced by a transformed eukaryotic cell line comprising an expression  
5 vector for producing said anhydrase and wherein said vector has a cloned bacterial organophosphorus acid anhydrase gene fragment with the DNA coding sequence:

```
5'
CTGCAGCGCTGACTCGGACCACTGCGCTGCAAGCAGAGTCTGTAAGCAATCCCAAGGGGGCAGC
ATG CAA ACG AGA AGG GTT GTG CTC AAG TCT GCG GCC GCA GGA ACT CTG CTC GGC
met gln thr arg arg val val leu lys ser ala ala ala gly thr leu leu gly
GCC CTG GCT GCG TCG GCG AGC TCG CTC GAT CGA TCG GCA CAG GCG ATC GGA TCA
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser
ATA CGT GCG CGT CCT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTG ACT CAC GAG
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his glu
GAC ATC TGG GCG AGC TCG GCA GGA TTC TTC CGT GCT TGG CCA GAG TTC TTC GGT
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly
AGC CGC AAA GCT CTA GCG GAA AAG GCT GCG AGA GGA TTG CGC GCC AGA GCG GCT
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala
GCC CTG CGA ACG ATT GTC GAT GTG TCG ACT TCG GAT ATC GGT CGC GAC GTC AGT
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser
TTA TTG GCC GAG GTT TCG CGG GCT GCG GAC GTT CAT ATC GTG GCG GCC ACC GCG
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly
TTG TGG TTC GAC CCG CCA CTT TCG ATG CGA TTG AGG TAT GTA GAG GAA CTC ACA
leu trp phe asp pro pro leu ser met arg leu arg tyr val glu glu leu thr
CAG TTC TTC CTG GGT GAG ATT CAA TAT GCG ATC GAA GAC ACC GGA ATT AGG GCG
gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala
GCC ATT ATC AAG GTG GCG ACC ACA GCG AAG GCG ACC CGC TTT CAG GAG TTA GTG
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val
TTA AAG GCG GCC GCG CCG GCG AGC TTG GCG ACC GGT GTT CCG GTA ACC AGT CAC
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his
ACG GCA GCA AGT CAG CCG GAT GGT GAG CGA GCG AGG CCG CCA TTT TTG AGT CCG
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro
AAG CTT GAG CCG TCA CCG GTT TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTG
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp asp leu
AGC TAT CTC ACC GCG CAG CTC CCG GGA TAC CTC ATC GGT CTA GAC CAC ATC CCG
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro
CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CCG CTC CTC GCG ATC
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile
CGT TCG TGG CAA ACA CCG GCT CTC TTG ATC AAG GCG CTC ATC GAC CAA GCG TAC
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr
ATG AAA CAA ATC CTC GTT TCG AAT GAC TCG CTC TTC GCG TTT TCG AGC TAT GTC
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val
ACC AAC ATC ATG GAC GTG ATG GAT CCG GTG AAC CCC GAC GCG ATG GCG TTC ATT
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile
CCA CTC AGA GTG ATC CCA TTT TAC GAG AGA AGG GCG TCC CAC AGG AAA CCG TCG
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys
CAG GCA TCA CTC TGA
gln ala ser leu
CTAACCGGGCGCGTTCTGTGTGTCACCGAAGTTCGCGTGCATGACGCCATCTGGATCTTCCACCGAGCGCGCC
ACTATTCCCGCTGTAAGATACCGAAGCATGAAGTCCGCGCATCGATAGGCATCTTCAATGTGATCAGGG
CTGCCAGCTCCAAAGCCGGGTGGCCACCCCTGTGCGATAGTCTTGAGGGACGGTAGCGGACCGCTGCTTTTC
GTGAACGCGAG
3'
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63. The method of claim 53 wherein said recombinant bacterial organophosphorus acid anhydase is produced by a transgenic eukaryotic organism comprising an expression vector for producing said anhydase wherein said vector
- 5 has a cloned bacterial organophosphorus acid anhydase gene fragment with the DNA coding sequence:

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5'
CTSCAGCCTGACTCGGACCCAGTCCGCTSCAGCAGAGTCCSTAAGCAATCGCAAGGGGGCAGC
ATG CAA ACG AGA AGG GAT GTG CTC AAG TCG GCG GCC GCA GGA ACT CTC CTC GGC
met gln thr arg arg val val leu lys ser ala ala ala gly thr leu leu gly
GGC CTC GGT GGA TGC GCG ACG TCG CTC GAT CGA TCG GCA CAG GCG ATC GGA TCA
gly leu ala gly cys ala thr trp leu asp arg ser ala gln ala ile gly ser
ATA CGT GCG CGT CCT ATC ACA ATC TCT GAA GCG GGT TTC ACA CTC ACT CAC GAG
ile arg ala arg pro ile thr ile ser glu ala gly phe thr leu thr his gly
GAC ATC TCG GCG AGC TCG GCA GGA TTC TCG CGT GCT TCG CCA GAG TTC TTC GGT
asp ile cys gly ser ser ala gly phe leu arg ala trp pro glu phe phe gly
AGC CGC AAA GCT CTA GCG GAA AAG GCT GTG AGA GGA TTC CGC GCC AGA GCG GGT
ser arg lys ala leu ala glu lys ala val arg gly leu arg ala arg ala ala
GGC GTG CGA ACG ATT GTC GAT GTC TCG ACT TTC GAT ATC GGT CGC GAC GTC AGT
gly val arg thr ile val asp val ser thr phe asp ile gly arg asp val ser
TTA TTC GCC GAG GTT TCG CGG GCT GCC GAC GTT CAT ATC GTG GCG GCG ACC GGC
leu leu ala glu val ser arg ala ala asp val his ile val ala ala thr gly
TTC TCG TTC GAC CGC CCA CTT TCG ATC CGA TTC AGG TAT GTA GAG GAA CTC ACA
leu trp phe asp pro leu ser met arg leu arg tyr val glu glu leu thr
CAG TTC TTC GTC CGT GAG ATT CAA TAT GGC ATC GAA GAC ACC GGA ATT AGG GCG
gln phe phe leu arg glu ile gln tyr gly ile glu asp thr gly ile arg ala
GGC ATT ATC AAG GTC GCG ACC ACA GCG AAG GCG ACC CGC TTT CAG GAG TTA GTC
gly ile ile lys val ala thr thr gly lys ala thr pro phe gln glu leu val
TTA AAG GCG GCT GCC CGG GCG ACC TTC GCG ACC GGT GTT CGC GTA ACC ACT CAC
leu lys ala ala ala arg ala ser leu ala thr gly val pro val thr thr his
ACG GCA GCA AGT CAG CCC GAT GGT CAG CGA GCG AGG CGC CCA TTT TTC AGT CGC
thr ala ala ser gln arg asp gly glu arg gly arg pro pro phe leu ser pro
AAG CTT GAG CGC TCA GCG GTC TGT ATT GGT CAC AGC GAT GAT ACT GAC GAT TTC
lys leu glu pro ser arg val cys ile gly his ser asp asp thr asp leu
AGC TAT CTC ACC GCG CTC CTC GCG GGA TAC CTC ATC GGT GTA GAC CAC ATC CGC
ser tyr leu thr ala leu leu arg gly tyr leu ile gly leu asp his ile pro
CAC AGT GCG ATT GGT CTA GAA GAT AAT GCG AGT GCA TCA CGC CTC CTC GCG ATC
his ser ala ile gly leu glu asp asn ala ser ala ser pro leu leu gly ile
CGT TCG TCG CAA ACA CGG GCT CTC TTC ATC AAG GCG CTC ATC GAC CAA GCG TAC
arg ser trp gln thr arg ala leu leu ile lys ala leu ile asp gln gly tyr
ATG AAA CAA ATC CTC GTT TCG AAT GAC TGG CTC TTC GCG TTT TCG AGC TAT GTC
met lys gln ile leu val ser asn asp trp leu phe gly phe ser ser tyr val
ACC AAC ATC ATC GAC GTC ATG GAT CGC GTC AAC CGC GAC GCG ATG GCG TTC ATT
thr asn ile met asp val met asp arg val asn pro asp gly met ala phe ile
CCA CTC AGA GTC ACC CCA TTC TAC GAG AGA AGC GCG TCC CAC AGG AAA CGC TCG
pro leu arg val ile pro phe tyr glu arg arg ala ser his arg lys arg cys
CAG GCA TCA CTC TGA
gln ala ser leu
CTAACCCCGGCGCGGTCTGTGTCCACCGAATTGCGCGTGCATGACGCCCATCTGGATCCTTCCACCGCAGCGGCG
ACTATTCGCGCTCAAGATACCGAACCGATGAAGTCCGCGCATCGATCGATAGGCATCTTCAATGTGATCAGGG
CTGCCACCTCCAAAGCGCGGTGGCCACCCCTGTCTGATAGTCTTTAGGGGACGGTAGCGACGCGCTGCTTTTC
GTGAAGTCCAG
3'
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64. A method of preventing poisoning of a locus by an organophosphorus compound by applying recombinant organophosphorus acid anhydrase to said locus before said compound contacts said locus.

5

65. A method of detecting bacterial colonies capable of detoxifying organophosphorus acid anhydrides, comprising employing a transformed microorganism as a control in a plate assay wherein said microorganism is comprised of an expression vector for producing organophosphorus acid anhydrase and said vector is comprised of a cloned gene fragment containing the DNA coding sequence for the anhydrase.

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66. The method of claim 65 wherein said anhydrides comprise a pesticide and said plate assay is conducted prior to applying said pesticide to soil to quantitate the number of microorganisms capable of detoxifying said pesticides in said soil.

67. A method for protecting insects from organophosphorus compounds comprising feeding said insects recombinant organophosphorus acid anhydrase.

68. A method for protecting insects from organophosphorus compounds comprising infecting insects with microorganisms comprised of an expression vector for producing an organophosphorus acid anhydrase wherein said vector is comprised of a cloned gene fragment containing the DNA coding sequence for the anhydrase.

69. A method for protecting insects from organophosphorus compounds comprising introducing into the environment of said insects microorganisms comprised of an expression vector for producing an organophosphorus acid anhydrase  
5 wherein said vector is comprised of a cloned gene fragment containing the DNA coding sequence of the anhydrase.

70. A pesticide comprising an organophosphorus compound  
10 and an inhibitor of bacterial organophosphorus acid anhydrase.

*add  
a<sub>4</sub>*

*add E2*

*add E2*